## AMENDMENTS TO THE CLAIMS

**This listing of claims will replace all prior versions and listings of claims in the application:**

## LISTING OF CLAIMS:

1.-19. **(Canceled).**

20. **(Currently amended)** A method for identifying a candidate protein useful as an anti-infective, comprising:

(a) calculating computationally protein sequence-based attributes from protein sequences of a pathogenic organism, wherein said protein sequences are predicted from whole genomic sequences or are predicted from partial genomic sequences comprising at least one chromosome, and wherein said protein sequence-based attributes are selected from a group consisting of percentage of charged amino acids, percentage hydrophobicity, distance of protein sequence from a fixed reference frame, measure of dipeptide complexity, and measure of hydrophobicity from a fixed reference frame;

(b) clustering computationally said protein sequences based on said protein sequence-based attributes using Principle Component Analysis, and displaying the results of said clustering;

(c) identifying computationally outlier proteins, wherein said outlier proteins appear outside a main cluster;

(d) comparing outlier proteins with protein sequences in databases;

(e)(d) selecting an outlier protein for further testing as an anti-infective; and

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(f)(e) validating said outlier protein as an anti-infective.

21.    (Previously presented)  The method of claim 20, wherein said pathogenic organism is selected from the group consisting of *B.burgdorfei, C.jejuni, C.pneumoniae, C.trachomatis, H.influenzae, H.pylori, L.major, M.genitalium, M.pneumoniae, M.tuberculosis, N.menigitis, P.aeruginosa, P.falciparum, R.prowazekii, T.pallidum,* and *V.cholerae.*

22.    (Previously presented)  The method of claim 20, wherein said protein sequence-based attributes are selected from the group consisting of fixed protein attributes and variable protein attributes.

23.    (Previously presented)  The method of claim 22, wherein a variable protein attribute is a distance of protein sequence from a variable reference frame.

24.    (Previously presented)  The method of claim 20, wherein said clustering is done by Principle Component Analysis using correlation coefficient between said protein sequence-based attributes.

25.    (Canceled)

26.    (Previously presented) The method of claim 20, wherein said outlier protein is non-- homologous to known anti-infective proteins from a pathogen selected from the group consisting of *B.burgdorfei, C.jejuni, C.pneumoniae, C.trachomatis, H.influenzae, H.pylori, L.major, M.genitalium,*

*M.pneumoniae, M.tuberculosis, N.menigitis, P.aeruginosa, P.falciparum, R.prowazekii, T.pallidum,* and

*V.cholerae.*

27.     **(Previously presented)** The method of claim 20, wherein said outlier protein has an

amino acid sequence selected from the group consisting of SEQ ID Nos: 1-31.

28.     **(Previously presented)** The method of claim 20, wherein said outlier protein has an amino

acid sequence selected from the group consisting of SEQ ID Nos: 32-118.

29.     **(Previously presented)** The method of claim 20, wherein steps are performed by a

computer system comprising:

(1) a central processing unit (CPU), wherein said CPU executes DISTANCE program and

clusters protein sequences based on protein sequence-based attributes using Principle Component

Analysis, thereby producing results;

(2) a memory device accessed by said CPU, wherein said memory device stores said results;

(3) a display on which said CPU displays said results in response to user inputs; and

(4) a user interface device.

30.     **(Previously presented)** The method of claim 20, further comprising using said outlier

protein for a diagnostic purpose.

31.     **(Canceled)**

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32.     **(Previously presented)**  The method of claim 20, further comprising using said outlier protein for a therapeutic purpose.

33.     **(Previously presented)**  The method as of claim 20, wherein said outlier protein can elicit an immune response.